SEQUENCE LISTING

(1) GENERAL INFORMATION:

  (i) APPLICANT: Shak, Steven

 (ii) TITLE OF INVENTION: Anti-Infective Therapy

(iii) NUMBER OF SEQUENCES: 25

 (iv) CORRESPONDENCE ADDRESS:
     (A) ADDRESSEE: Genentech, Inc.
     (B) STREET: 1 DNA Way
     (C) CITY: South San Francisco
     (D) STATE: California
     (E) COUNTRY: USA
     (F) ZIP: 94080

  (v) COMPUTER READABLE FORM:
     (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
     (B) COMPUTER: IBM PC compatible
     (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     (D) SOFTWARE: WinPatin (Genentech)

 (vi) CURRENT APPLICATION DATA:
     (A) APPLICATION NUMBER: To Be Assigned
     (B) FILING DATE: 07-Nov-2001
     (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
     (A) APPLICATION NUMBER: 09/669306
     (B) FILING DATE: 25-Sep-2001

(vii) PRIOR APPLICATION DATA:
     (A) APPLICATION NUMBER: 08/873506
     (B) FILING DATE: 08-Dec-1999

(vii) PRIOR APPLICATION DATA:
     (A) APPLICATION NUMBER: 08/643195
     (B) FILING DATE: 06-May-1996

(vii) PRIOR APPLICATION DATA:
     (A) APPLICATION NUMBER: 08/459909
     (B) FILING DATE: 02-Jun-1995

(vii) PRIOR APPLICATION DATA:

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        (A)  APPLICATION NUMBER: 08/191749
        (B)  FILING DATE: 03-Feb-1994

   (vii)  PRIOR APPLICATION DATA:
        (A)  APPLICATION NUMBER: 07/914,226
        (B)  FILING DATE: 13-Jul-1992

   (vii)  PRIOR APPLICATION DATA:
        (A)  APPLICATION NUMBER: 07/448038
        (B)  FILING DATE: 08-Dec-1989

   (vii)  PRIOR APPLICATION DATA:
        (A)  APPLICATION NUMBER: 07/289958
        (B)  FILING DATE: 23-Dec-1988

  (viii)  ATTORNEY/AGENT INFORMATION:
        (A)  NAME: Johnston, Sean A.
        (B)  REGISTRATION NUMBER: 35,910
        (C)  REFERENCE/DOCKET NUMBER: P0530P1C10

    (ix)  TELECOMMUNICATION INFORMATION:
        (A)  TELEPHONE: 650/225-3562
        (B)  TELEFAX: 650/952-9881
(2)  INFORMATION FOR SEQ ID NO:1:

    (i)  SEQUENCE CHARACTERISTICS:
        (A)  LENGTH: 51 base pairs
        (B)  TYPE: Nucleic Acid
        (C)  STRANDEDNESS: Single
        (D)  TOPOLOGY: Linear

   (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:1:


GTGCTGGACA CCTACCAGTA TGATGATGGC TGTGAGTCCT GTGGCAATGA 50

C 51

(2)  INFORMATION FOR SEQ ID NO:2:

    (i)  SEQUENCE CHARACTERISTICS:
        (A)  LENGTH: 17 amino acids
        (B)  TYPE: Amino Acid
        (D)  TOPOLOGY: Linear

   (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:2:
```

2

```
Val Leu Asp Thr Tyr Gln Tyr Asp Asp Gly Cys Glu Ser Cys Gly
 1               5                  10                      15
```

Asn Asp

(2) INFORMATION FOR SEQ ID NO:3:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 71 base pairs
      (B) TYPE: Nucleic Acid
      (C) STRANDEDNESS: Single
      (D) TOPOLOGY: Linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TATGACGTCT ACCTGGACGT GCAGCAGAAG TGGCATCTGA ATGATGTGAT 50

GCTGATGGGC GACTTCAACG C 71

(2) INFORMATION FOR SEQ ID NO:4:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 23 amino acids
      (B) TYPE: Amino Acid
      (D) TOPOLOGY: Linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Tyr Asp Val Tyr Leu Asp Val Gln Gln Lys Trp His Leu Asn Asp
 1               5                  10                      15
```

```
Val Met Leu Met Gly Asp Phe Asn
                20
```

(2) INFORMATION FOR SEQ ID NO:5:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 42 base pairs
      (B) TYPE: Nucleic Acid
      (C) STRANDEDNESS: Single
      (D) TOPOLOGY: Linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTGAAGATCG CAGCCTTCAA CATCCAGACA TTTGGGGAGA CC 42

(2) INFORMATION FOR SEQ ID NO:6:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 42 base pairs
       (B) TYPE: Nucleic Acid
       (C) STRANDEDNESS: Single
       (D) TOPOLOGY: Linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCCGCATGTC CCAGGGCCAC AGGCAGCGTT TCCTGGTAGG AC 42

(2) INFORMATION FOR SEQ ID NO:7:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 31 base pairs
       (B) TYPE: Nucleic Acid
       (C) STRANDEDNESS: Single
       (D) TOPOLOGY: Linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTGAAGATCG CAGCCTTCAA CATCCAGACA T 31

(2) INFORMATION FOR SEQ ID NO:8:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 31 base pairs
       (B) TYPE: Nucleic Acid
       (C) STRANDEDNESS: Single
       (D) TOPOLOGY: Linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTGGATGTTG AAGGVTGCGA TCTTCAATGC A 31

(2) INFORMATION FOR SEQ ID NO:9:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 42 base pairs
       (B) TYPE: Nucleic Acid

```
         (C) STRANDEDNESS: Single
         (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:


CTAGAATTAT GTTAAAAATT GCAGCATTTA ATATTCAAAC AT 42

(2) INFORMATION FOR SEQ ID NO:10:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 34 base pairs
         (B) TYPE: Nucleic Acid
         (C) STRANDEDNESS: Single
         (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:


TTGAATATTA AATGCTGCAA TTTTTAACAT AATT 34

(2) INFORMATION FOR SEQ ID NO:11:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 7 amino acids
         (B) TYPE: Amino Acid
         (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Leu Lys Ile Ala Ala Phe
  1               5

(2) INFORMATION FOR SEQ ID NO:12:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 1039 base pairs
         (B) TYPE: Nucleic Acid
         (C) STRANDEDNESS: Double
         (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:


TCCTGCACAG GCAGTGCCTT GAAGTGCTTC TTCAGAGACC TTTCTTCATA 50
```

5

GACTACTTTT TTTTCTTTAA GCAGCAAAAG GAGAAAATTG TCATCAAAGG 100

ATATTCCAGA TTCTTGACAG CATTCTCGTC ATCTCTGAGG ACATCACCAT 150

CATCTCAGGA TGAGGGGCAT GAAGCTGCTG GGGGCGCTGC TGGCACTGGC 200

GGCCCTACTG CAGGGGGCCG TGTCCCTGAA GATCGCAGCC TTCAACATCC 250

AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT 300

GTGCAGATCC TGAGCCGCTA TGACATCGCC CTGGTCCAGG AGGTCAGAGA 350

CAGCCACCTG ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGATG 400

CACCAGACAC CTATCACTAC GTGGTCAGTG AGCCACTGGG ACGGAACAGC 450

TATAAGGAGC GCTACCTGTT CGTGTACAGG CCTGACCAGG TGTCTGCGGT 500

GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG AACGACACCT 550

TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC 600

AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC 650

CGAGATCGAC GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG 700

GCTTGGAGGA CGTCATGTTG ATGGGCGACT TCAATGCGGG CTGCAGCTAT 750

GTGAGACCCT CCCAGTGGTC ATCCATCCGC CTGTGGACAA GCCCCACCTT 800

CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA CCCACGCACT 850

GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGCGCCGTT 900

GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG 950

TGACCAACTG GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC 1000

TGAAGTGAGC AGCCCCTCCC CACACCAGTT GAACTGCAG 1039

(2) INFORMATION FOR SEQ ID NO:13:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 341 amino acids
       (B) TYPE: Amino Acid
       (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
Ser Cys Thr Gly Ser Ala Leu Lys Cys Phe Phe Arg Asp Leu Ser
 1               5                  10                  15

Ser Thr Thr Phe Phe Ser Leu Ser Ser Lys Arg Arg Lys Leu Ser
                20                  25                  30

Ser Lys Asp Ile Pro Asp Ser Gln His Ser Arg His Leu Gly His
                35                  40                  45

His His His Leu Arg Met Arg Gly Met Lys Leu Leu Gly Ala Leu
                50                  55                  60

Leu Ala Leu Ala Ala Leu Leu Gln Gly Ala Val Ser Leu Lys Ile
                65                  70                  75

Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys Met Ser Asn
                80                  85                  90

Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp
                95                  100                 105

Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val
                110                 115                 120

Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr
                125                 130                 135

His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu
                140                 145                 150

Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp
                155                 160                 165

Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr
                170                 175                 180

Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr
                185                 190                 195

Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly
                200                 205                 210

Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp
                215                 220                 225
```

7

```
Val Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp
                230                 235                 240

Phe Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser
                245                 250                 255

Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp
                260                 265                 270

Ser Ala Asp Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg
                275                 280                 285

Ile Val Val Ala Gly Met Leu Leu Arg Gly Ala Val Val Pro Asp
                290                 295                 300

Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr Gly Leu Ser Asp
                305                 310                 315

Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val Glu Val Met
                320                 325                 330

Leu Lys Ala Ala Pro Pro His Thr Ser Thr Ala
                335                 340
```

(2) INFORMATION FOR SEQ ID NO:14:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 260 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys
  1               5                  10                  15

Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser
                20                  25                  30

Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu
                35                  40                  45

Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro
                50                  55                  60
```

```
Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser
                65                  70                  75

Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser
                80                  85                  90

Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly
                95                 100                 105

Asn Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser
               110                 115                 120

Arg Phe Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala
               125                 130                 135

Ala Pro Gly Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val
               140                 145                 150

Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu
               155                 160                 165

Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln
               170                 175                 180

Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu
               185                 190                 195

Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr His Cys Ala
               200                 205                 210

Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly Ala Val
               215                 220                 225

Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr Gly
               230                 235                 240

Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val
               245                 250                 255

Glu Val Met Leu Lys
               260
```

(2) INFORMATION FOR SEQ ID NO:15:

    (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
Leu Lys Ile Ala Ala Phe Asn Ile Arg Thr Phe Gly Glu Thr Lys
 1               5                  10                  15

Met Ser Asn Ala Thr Leu Ala Ser Tyr Ile Val Arg Ile Val Arg
                20                  25                  30

Arg Tyr Asp Ile Val Leu Ile Glu Gln Val Arg Asp Ser His Leu
                35                  40                  45

Val Ala Val Gly Lys Leu Leu Asp Tyr Leu Asn Gln Asp Asp Pro
                50                  55                  60

Asn Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser
                65                  70                  75

Tyr Lys Glu Arg Tyr Leu Phe Leu Phe Arg Pro Asn Lys Val Ser
                80                  85                  90

Val Leu Asp Thr Tyr Gln Tyr Asp Asp Gly Cys Glu Ser Cys Gly
                95                  100                 105

Asn Asp Ser Phe Ser Arg Glu Pro Ala Val Val Lys Phe Ser Ser
                110                 115                 120

His Ser Thr Lys Val Lys Glu Phe Ala Ile Val Ala Leu His Ser
                125                 130                 135

Ala Pro Ser Asp Ala Val Ala Glu Ile Asn Ser Leu Tyr Asp Val
                140                 145                 150

Tyr Leu Asp Val Gln Gln Lys Trp His Leu Asn Asp Val Met Leu
                155                 160                 165

Met Gly Asp Phe Asn Ala Asp Cys Ser Tyr Val Thr Ser Ser Gln
                170                 175                 180

Trp Ser Ser Ile Arg Leu Arg Thr Ser Ser Thr Phe Gln Trp Leu
                185                 190                 195

Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Ser Thr Asn Cys Ala
```

10

```
            200                      205                      210
```

Tyr Asp Arg Ile Val Val Ala Gly Ser Leu Leu Gln Ser Ser Val
                215   220   225

Val Gly Pro Ser Ala Ala Pro Phe Asp Phe Gln Ala Ala Tyr Gly
                230   235   240

Leu Ser Asn Glu Met Ala Leu Ala Ile Ser Asp His Tyr Pro Val
                245   250   255

Glu Val Thr Leu Thr
                260

(2) INFORMATION FOR SEQ ID NO:16:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 664 base pairs
      (B) TYPE: Nucleic Acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTCGAGCTCG CCCGACATTG ATTATTGACT AGAGTCGACA GCTGTGGAAT 50

GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG CAGGCAGAAG 100

TATGCAAAGC ATGCATCTCA ATTAGTCAGC AACCAGGTGT GGAAAGTCCC 150

CAGGCTCCCC AGCAGGCAGA AGTATGCAAA GCATGCATCT CAATTAGTCA 200

GCAACCATAG TCCCGCCCCT AACTCCGCCC ATCCCGCCCC TAACTCCGCC 250

CAGTTCCGCC CATTCTCCGC CCCATGGCTG ACTAATTTTT TTTATTTATG 300

CAGAGGCCGA GGCCGCCTCG GCCTCTGAGC TATTCCAGAA GTAGTGAGGA 350

GGCTTTTTTG GAGGCCTAGG CTTTTGCAAA AAGCTTATCG GCCGGGAAC 400

GGTGCATTGG AACGCGGATT CCCCGTGCCA AGAGTGACGT AAGTACCGCC 450

TATAGAGTCT ATAGGCCCAC CCCCTTGGCT TCGTTAGAAC GCGGCTACAA 500

TTAATACATA ACCTTATGTA TCATACACAT ACGATTTAGG TGACACTATA 550
```

11

GAATAACATC CACTTTGCCT TTCTCTCCAC AGGTGTCCAC TCCCAGGTCC 600

AACTGCACCT CGGTTCTAAG CTTGGGCTGC AGGTCGCCGT GAATTTAAGG 650

GACGCTGTGA AGCA 664

(2) INFORMATION FOR SEQ ID NO:17:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 664 base pairs
       (B) TYPE: Nucleic Acid
       (C) STRANDEDNESS: Double
       (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TTCGAGCTCG CCCGACATTG ATTATTGACT AGAGTCGACA GCTGTGGAAT 50

GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG CAGGCAGAAG 100

TATGCAAAGC ATGCATCTCA ATTAGTCAGC AACCAGGTGT GGAAAGTCCC 150

CAGGCTCCCC AGCAGGCAGA AGTATGCAAA GCATGCATCT CAATTAGTCA 200

GCAACCATAG TCCCGCCCCT AACTCCGCCC ATCCCGCCCC TAACTCCGCC 250

CAGTTCCGCC CATTCTCCGC CCCATGGCTG ACTAATTTTT TTTATTTATG 300

CAGAGGCCGA GGCCGCCTCG GCCTCTGAGC TATTCCAGAA GTAGTGAGGA 350

GGCTTTTTTG GAGGCCTAGG CTTTTGCAAA AAGCTTATCC GGCCGGGAAC 400

GGTGCATTGG AACGCGGATT CCCCGTGCCA AGAGTCAGGT AAGTACCGCC 450

TATAGAGTCT ATAGGCCCAC CCCCTTGGCT TCGTTAGAAC GCGGCTACAA 500

TTAATACATA ACCTTATGTA TCATACACAT ACGATTTAGG TGACACTATA 550

GAATAACATC CACTTTGCCT TTCTCTCCAC AGGTGTCCAC TCCCAGGTCC 600

AACTGCACCT CGGTTCTAAG CTTGGGCTGC AGGTCGCCGT GAATTTAAGG 650

GACGCTGTGA AGCA 664

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 640 base pairs
    (B) TYPE: Nucleic Acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```
TTCGAGCTCG CCCGACATTG ATTATTGACT AGAGTCGACA GCTGTGGAAT 50

GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG CAGGCAGAAG 100

TATGCAAAGC ATGCATCTCA ATTAGTCAGC AACCAGGTGT GGAAAGTCCC 150

CAGGCTCCCC AGCAGGCAGA AGTATGCAAA GCATGCATCT CAATTAGTCA 200

GCAACCATAG TCCCGCCCCT AACTCCGCCC ATCCCGCCCC TAACTCCGCC 250

CAGTTCCGCC CATTCTCCGC CCCATGGCTG ACTAATTTTT TTTATTTATG 300

CAGAGGCCGA GGCCGCCTCG GCCTCTGAGC TATTCCAGAA GTAGTGAGGA 350

GGCTTTTTTG GAGGCCTAGG CTTTTGCAAA AAGCTTATCC GGCCGGGAAC 400

GGTGCATTGG AACGCGGATT CCCCGTGCCA AGAGTCAGGT AAGTACCGCC 450

TATAGAGTCT ATAGGCCCAC CCCCTTGGCT TCGTTAGAAC GCGGCTACAA 500

TTAATACATA ACCTTTTGGA TCCTATAGAC TGACATCCAC TTTGCCTTTC 550

TCTCCACAGG TGTCCACTCC CAGGTCCAAC TGCACCTCGG TTCGAAGCTT 600

GGGCTGCAGG TCGCCGTGAA TTTAAGGGAC GCTGTGAAGC 640
```

(2) INFORMATION FOR SEQ ID NO:19:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 646 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Double
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

13

```
TTCGAGCTCG CCCGACATTG ATTATTGACT AGAGTCGACA GCTGTGGAAT 50

GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG CAGGCAGAAG 100

TATGCAAAGC ATGCATCTCA ATTAGTCAGC AACCAGGTGT GGAAAGTCCC 150

CAGGCTCCCC AGCAGGCAGA AGTATGCAAA GCATGCATCT CAATTAGTCA 200

GCAACCATAG TCCCGCCCCT AACTCCGCCC ATCCCGCCCC TAACTCCGCC 250

CAGTTCCGCC CATTCTCCGC CCCATGGCTG ACTAATTTTT TTTATTTATG 300

CAGAGGCCGA GGCCGCCTCG GCCTCTGAGC TATTCCAGAA GTAGTGAGGA 350

GGCTTTTTTG GAGGCCTAGG CTTTTGCAAA AAGCTTATCC GGCCGGGAAC 400

GGTGCATTGG AACGCGGATT CCCCGTGCCA AGAGTCAGGT AAGTACCGCC 450

TATAGAGTCT ATAGGCCCAC CCCCTTGGCT TCGTTAGAAC GCGGCTACAA 500

TTAATACATA ACCTTTTGGA TCCTACTAAC TACTGACTTA TTCTTTTCCT 550

TTCTCTCCAC AGGTGTCCAC TCCCAGGTCC AACTGCACCT CGGTTCGCGA 600

AGCTTGGGCT GCAGGTCGCC GTGAATTTAA GGGACGCTGT GAAGCA 646
```

(2) INFORMATION FOR SEQ ID NO:20:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 645 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Double
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
TTCGAGCTCG CCCGACATTG ATTATTGACT AGAGTCGACA GCTGTGGAAT 50

GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG CAGGCAGAAG 100

TATGCAAAGC ATGCATCTCA ATTAGTCAGC AACCAGGTGT GGAAAGTCCC 150

CAGGCTCCCC AGCAGGCAGA AGTATGCAAA GCATGCATCT CAATTAGTCA 200

GCAACCATAG TCCCGCCCCT AACTCCGCCC ATCCCGCCCC TAACTCCGCC 250
```

14

CAGTTCCGCC CATTCTCCGC CCCATGGCTG ACTAATTTTT TTTATTTATG 300

CAGAGGCCGA GGCCGCCTCG GCCTCTGAGC TATTCCAGAA GTAGTGAGGA 350

GGCTTTTTTG GAGGCCTAGG CTTTTGCAAA AAGCTTATCC GGCCGGGAAC 400

GGTGCATTGG AACGCGGATT CCCCGTGCCA AGAGTCAGGT AAGTACCGCC 450

TATAGAGTCT ATAGGCCCAC CCCCTTGGCT TCGTTAGAAC GCGGCTACAA 500

TTAATACATA ACCTTTTGGA TCCTACTGAC ACTGACATCC ACTTTTTCTT 550

TTTCTCCACA GGTGTCCACT CCCAGGTCCA ACTGCACCTC GGTTCGCGAA 600

GCTTGGGCTG CAGGTCGCCG TGAATTTAAG GGACGCTGTG AAGCA 645

(2) INFORMATION FOR SEQ ID NO:21:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 81 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TGACGTAAGT ACATGTATCA TACACATACG ATTTAGGTGA CACTATAGAA 50

TAACATCCAC TTTGCCTTTC TCTCCACAGG T 81

(2) INFORMATION FOR SEQ ID NO:22:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 81 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TCAGGTAAGT ACATGTATCA TACACATACG ATTTAGGTGA CACTATAGAA 50

TAACATCCAC TTTGCCTTTC TCTCCACAGG T 81

15

(2) INFORMATION FOR SEQ ID NO:23:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 58 base pairs
      (B) TYPE: Nucleic Acid
      (C) STRANDEDNESS: Single
      (D) TOPOLOGY: Linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TCAGGTAAGT ACTTGGATCC TATAGACTGA CATCCACTTT GCCTTTCTCT 50

CCACAGGT 58

(2) INFORMATION FOR SEQ ID NO:24:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 61 base pairs
      (B) TYPE: Nucleic Acid
      (C) STRANDEDNESS: Single
      (D) TOPOLOGY: Linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TCAGGTAAGT ACTTGGATCC TACTAACTAC TGACTTATTC TTTTCCTTTC 50

TCTCCACAGG T 61

(2) INFORMATION FOR SEQ ID NO:25:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 60 base pairs
      (B) TYPE: Nucleic Acid
      (C) STRANDEDNESS: Single
      (D) TOPOLOGY: Linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TCAGGTAAGT ACTTGGATCC TACTGACACT GACATCCACT TTTTCTTTTT 50

CTCCACAGGT 60